IN THE SPECIFICATION

At page 1, please replace lines 3-9 with the following text:

This application is a divisional of U.S. Patent Application Serial No. 09/261,599, filed February 26, 1999, now granted as U.S. Patent No. 6,395,877, which is a continuation-in-part of ~~copending~~ U.S. Patent Application Serial No. 09/223,538, filed December 30, 1998, now abandoned, ~~and entitled "14273 RECEPTOR, A NOVEL G-PROTEIN COUPLED RECEPTOR" (Attorney's Docket No. 5800-4A),~~ which is a continuation-in-part of ~~copending~~ U.S. Patent Application Serial No. 09/107,761, filed June 30, 1998, ~~and entitled "14273 RECEPTOR, A NOVEL G-PROTEIN COUPLED RECEPTOR" (Attorney's Docket No. 5800-4),~~ now abandoned, which are hereby incorporated herein in their entirety by reference.

At pages 4-5, please replace page 4, line 17 through page 5, line 3 with the following text:

The invention provides isolated 14273 receptor polypeptides including a polypeptide having the amino acid sequence shown in SEQ ID NO:1 ~~SEQ ID NO 1~~ (human) and SEQ ID NO:4 ~~SEQ ID NO 4~~ (murine), or the amino acid sequence encoded by the cDNA deposited as ATCC No. PTA-1143 ~~_____ on _____~~ ("the deposited cDNA").

The invention also provides isolated 14273 receptor nucleic acid molecules having the sequence shown in SEQ ID NO:2 ~~SEQ ID NO 2~~ (human) and SEQ ID NO:5 ~~SEQ ID NO 5~~ (murine) or in the deposited cDNA.

The invention also provides variant polypeptides having an amino acid sequence that is substantially homologous to the amino acid sequence shown in SEQ ID NO:1 ~~SEQ ID NO 1~~ or SEQ ID NO:4 ~~SEQ ID NO~~ 4 or encoded by the deposited cDNA.

The invention also provides variant nucleic acid sequences that are substantially homologous to the nucleotide sequence shown in SEQ ID NO:2 ~~SEQ ID NO 2~~ or SEQ ID NO:5 ~~SEQ ID NO 5~~ or in the deposited cDNA.

The invention also provides fragments of the polypeptide shown in SEQ ID NO:1 ~~SEQ ID NO 1~~ or SEQ ID NO:4 ~~SEQ ID NO 4~~ and nucleotide shown in SEQ ID NO:2 ~~SEQ ID NO 2~~ or SEQ ID NO:5 ~~SEQ ID NO 5~~, as well as substantially homologous fragments of the polypeptide or nucleic acid.

At pages 6-7, please replace page 6, line 24 through page 7, line 22, with the following text:

Figure 1 shows the human 14273 nucleotide sequence (SEQ ID NO:2~~SEQ ID NO 2~~) and the deduced 14273 amino acid sequence (SEQ ID NO:1~~SEQ ID NO 1~~). It is predicted that amino acids 1-45 of SEQ ID NO:1 constitute the amino terminal extracellular domain, amino acids 46-321 of SEQ ID NO:1 constitute the region spanning the transmembrane domain, and amino acids 322-361 of SEQ ID NO:1 constitute the carboxy terminal intracellular domain. The transmembrane domain contains seven transmembrane segments, three extracellular loops and three intracellular loops. The transmembrane segments are found from about amino acid 46 to about amino acid 66, from about amino acid 75 to about amino acid 98, from about amino acid 113 to about amino acid 134, from about amino acid 156 to about amino acid 177, from about amino acid 209 to about amino acid 227, from about amino acid 266 to about amino acid 289, and from about amino acid 297 to about amino acid 321 of SEQ ID NO:1. Within the region spanning the entire transmembrane domain are three intracellular and three extracellular loops. The three intracellular loops are found from about amino acid 67 to about amino acid 74, from about amino acid 135 to about amino acid 155, and from about amino acid 228 to about amino acid 265 of SEQ ID NO:1. The three extracellular loops are found at from about amino acid 99 to about amino acid 112, from about amino acid 178 to about amino acid 208, and from about amino acid 290 to about amino acid 296 of SEQ ID NO:1.

The transmembrane domain includes a sequence, ERM, corresponding to the GPCR signal transduction signature, DRY, at residues 135-137 of SEQ ID NO:1. The sequence includes an arginine at residue 136 of SEQ ID NO:1, an invariant amino acid in GPCRs.

Figure 2 shows a comparison of the human 14273 receptor against the Prosite data base of protein patterns, specifically showing a high score against the seven transmembrane segment rhodopsin superfamily (SEQ ID NO:3~~SEQ ID NO 3~~). The underlined area shows a sequence corresponding to the GPCR signature, and specifically the position of an arginine residue, conserved in GPCRs. The most commonly conserved sequence is an aspartate, arginine, tyrosine (DRY) triplet. DRY is implicated in signal transduction. Arginine is invariant. Aspartate is conservatively placed in several GPCRs. In the present case, the arginine is found in the sequence ERM, which matches the position of DRY or invariant arginine in GPCRs of the rhodopsin superfamily of receptors.

At page 8, please replace lines 1- 11 with the following text:

Figure 5 shows an analysis of the human 14273 open reading frame for amino acids corresponding to specific functional sites. Glycosylation sites are found from about amino acids 21-24 and 322-325 of SEQ ID NO:1. A cyclic AMP- and cyclic GMP-dependent protein kinase phosphorylation site is found at about

amino acids 239-242 of SEQ ID NO:1. A protein kinase C phosphorylation site is found from about amino acids 237-239 and 350-352 of SEQ ID NO:1. A casein kinase II phosphorylation site is found from about amino acids 256-259 of SEQ ID NO:1. N-myristoylation sites are found from about amino acids 57-62, 72-77, and 343-348 of SEQ ID NO:1. An amidation site is found at about amino acids 150-153 of SEQ ID NO:1. A leucine zipper pattern is shown at about amino acids 106-127 of SEQ ID NO:1. In addition, amino acids corresponding in position to the GPCR signature and containing the invariant arginine are found in the sequence ERM at amino acids 135-137 of SEQ ID NO:1.

At pages 8-9, please replace page 8, line 18 through page 9, line 16 with the following text:

Figure 7 shows the murine ortholog of 14273 nucleotide sequence (SEQ ID NO:5~~SEQ ID NO 5~~) and the deduced 14273 amino acid sequence (SEQ ID NO:4~~SEQ ID NO 4~~). It is predicted that amino acids 1-45 of SEQ ID NO:4 constitute the amino terminal extracellular domain, amino acids 46-321 of SEQ ID NO:4 constitute the region spanning the transmembrane domain, and amino acids 322-361 of SEQ ID NO:4 constitute the carboxy terminal intracellular domain. The transmembrane domain contains seven transmembrane segments, three extracellular loops and three intracellular loops. The transmembrane segments are found from about amino acid 96 to about amino acid 66, from about amino acid 77 to about amino acid 98, from about amino acid 113 to about amino acid 134, from about amino acid 156 to about amino acid 177, from about amino acid 209 to about amino acid 227, from about amino acid 266 to about amino acid 289, and from about amino acid 297 to about amino acid 321 of SEQ ID NO:4. Within the region spanning the entire transmembrane domain are three intracellular and three extracellular loops. The three intracellular loops are found from about amino acid 67 to about amino acid 76, from about amino acid 135 to about amino acid 155, and from about amino acid 228 to about amino acid 265 of SEQ ID NO:4. The three extracellular loops are found at from about amino acid 99 to about amino acid 112, from about amino acid 178 to about amino acid 208, and from about amino acid 290 to about amino acid 296 of SEQ ID NO:4.

The transmembrane domain includes a sequence, ERM, corresponding to the GPCR signal transduction signature, DRY, at residues 135-137 of SEQ ID NO:4. The sequence includes an arginine at residue 136 of SEQ ID NO:4, an invariant amino acid in GPCRs.

Figure 8 shows a comparison of the murine 14273 receptor against the Prosite data base of protein patterns, specifically showing a high score against the seven transmembrane segment rhodopsin superfamily (SEQ ID NO:3~~SEQ ID NO 3~~). The underlined area shows a sequence corresponding to the GPCR signature, and specifically the position of an arginine residue, conserved in GPCRs. The most commonly conserved sequence is an aspartate, arginine, tyrosine (DRY) triplet. DRY is implicated in signal transduction. Arginine is invariant. Aspartate is conservatively placed in several GPCRs. In the present case, the arginine

is found in the sequence ERM, which matches the position of DRY or invariant arginine in GPCRs of the rhodopsin superfamily of receptors.

At pages 9-10, please replace page 9, line 25 through page 10, line 5 with the following text:

Figure 11 shows an analysis of the murine 14273 open reading frame for amino acids corresponding to specific functional sites. Glycosylation sites are found from about amino acids 21-24 and 322-325 of SEQ ID NO:4. A cyclic AMP- and cyclic GMP-dependent protein kinase phosphorylation site is found at about amino acids 239-242 of SEQ ID NO:4. A protein kinase C phosphorylation site is found from about amino acids 237-239 and 350-352 of SEQ ID NO:4. Casein kinase II phosphorylation sites are found from about amino acids 40-43 and 256-259 of SEQ ID NO:4. N-myristoylation sites are found from about amino acids 57-62, 72-77, and 343-348 of SEQ ID NO:4. An amidation site is found at about amino acids 150-153 of SEQ ID NO:4. A leucine zipper pattern is shown at about amino acids 106-127 of SEQ ID NO:4. In addition, amino acids corresponding in position to the GPCR signature and containing the invariant arginine are found in the sequence ERM at amino acids 135-137 of SEQ ID NO:4. A glycosaminoglycan attachment site is found at about amino acids 148-151 of SEQ ID NO:4.

At page 14, please replace lines 1-12 with the following text:

The invention thus relates to a novel GPCR having the deduced amino acid sequence shown in Figure 1 (SEQ ID NO:1~~SEQ ID NO 1~~) or having the amino acid sequence encoded by the deposited cDNA, ATCC No. PTA-1143——. The invention also relates to the mouse ortholog corresponding to the novel human GPCR having the deduced amino acid sequence shown in Figure 7 (SEQ ID NO:4~~SEQ ID NO 4~~) or having the amino acid sequence encoded by the deposited cDNA, ATCC No. PTA-1143——.

The deposit will be maintained under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms. The deposit is provided as a convenience to those of skill in the art and is not an admission that a deposit is required under 35 U.S.C. § 112. The deposited sequence, as well as the polypeptide encoded by the sequence, is incorporated herein by reference and controls in the event of any conflict, such as a sequencing error, with description in this application.

At page 14, please replace lines 23-27 with the following text:

The "14273 receptor polypeptide" or "14273 receptor protein" refers to the polypeptide in SEQ ID NO:1~~SEQ ID NO 1~~ or SEQ ID NO:4~~SEQ ID NO 4~~ or encoded by the deposited cDNA. The term "receptor protein" or "receptor polypeptide", however, further includes the numerous variants described herein, as well as fragments derived from the full length 14273 polypeptide and variants.

At page 15, please replace lines 1-20 with the following text:

The human 14273 polypeptide is a 361 residue protein exhibiting three main structural domains. The amino terminal extracellular domain is identified to be within residues 1 to about 45 in SEQ ID NO:1~~SEQ ID NO 1~~. The transmembrane domain is identified to be within residues from about 46 to about 321 in SEQ ID NO:1~~SEQ ID NO 1~~. The carboxy terminal intracellular domain is identified to be within residues from about 322 to 361 in SEQ ID NO:1~~SEQ ID NO 1~~. The transmembrane domain contains seven segments that span the membrane. The transmembrane segments are found from about amino acid 46 to about amino acid 66, from about amino acid 75 to about amino acid 98, from about amino acid 113 to about amino acid 134, from about amino acid 156 to about amino acid 177, from about amino acid 209 to about amino acid 227, from about amino acid 266 to about amino acid 289, and from about amino acid 297 to about amino acid 321 of SEQ ID NO:1. Within the region spanning the entire transmembrane domain are three intracellular and three extracellular loops. The three intracellular loops are found from about amino acid 67 to about amino acid 74, from about amino acid 135 to about amino acid 155, and from about amino acid 228 to about amino acid 265 of SEQ ID NO:1. The three extracellular loops are found at from about amino acid 99 to about amino acid 112, from about amino acid 178 to about amino acid 208, and from about amino acid 290 to about amino acid 296 of SEQ ID NO:1.

The transmembrane domain includes a GPCR signal transduction signature, ERM, at residues 135-137 of SEQ ID NO:1. The sequence includes an arginine at residue 136 of SEQ ID NO:1, an invariant amino acid in GPCRs.

At pages 16-17, please replace page 16, line 22 through page 17, line 10 with the following text:

In one embodiment, the receptor polypeptide comprises the amino acid sequence shown in SEQ ID NO:1~~SEQ ID NO 1~~ or SEQ ID NO:4~~SEQ ID NO 4~~. However, the invention also encompasses sequence variants. Variants include a substantially homologous protein encoded by the same genetic locus in an organism, i.e., an allelic variant. Variants also encompass proteins derived from other genetic loci in an organism, but having substantial homology to the 14273 receptor protein of SEQ ID NO:1~~SEQ ID NO 1~~ or SEQ ID NO:4~~SEQ ID NO 4~~. Variants also include proteins substantially homologous to the 14273 receptor

protein but derived from another organism, i.e., an ortholog. Variants also include proteins that are substantially homologous to the 14273 receptor protein that are produced by chemical synthesis. Variants also include proteins that are substantially homologous to the 14273 receptor protein that are produced by recombinant methods. It is understood, however, that variants exclude any amino acid sequences disclosed prior to the invention.

As used herein, two proteins (or a region of the proteins) are substantially homologous when the amino acid sequences are at least about 50-55%, 55-60%, typically at least about 70-75%, more typically at least about 80-85%, and most typically at least about 90-95% or more homologous. A substantially homologous amino acid sequence, according to the present invention, will be encoded by a nucleic acid sequence hybridizing to the nucleic acid sequence, or portion thereof, of the sequence shown in SEQ ID NO:2~~SEQ ID NO 2~~ or SEQ ID NO:5~~SEQ ID NO 5~~ under stringent conditions as more fully described below.

At pages 19-20, please replace page 19, line 3 through page 20, line 14 with the following text:

The comparison of sequences and determination of percent identity and similarity between two sequences can be accomplished using a mathematical algorithm. (*Computational Molecular Biology*, Lesk, A.M., ed., Oxford University Press, New York, 1988; *Biocomputing: Informatics and Genome Projects*, Smith, D.W., ed., Academic Press, New York, 1993; *Computer Analysis of Sequence Data, Part 1*, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, 1994; *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987; and *Sequence Analysis Primer*, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991). In a preferred embodiment, the percent identity between two amino acid sequences is determined using the Needleman and Wunsch (*J. Mol. Biol.* (48):444-453 (1970)) algorithm which has been incorporated into the GAP program in the GCG software package ~~(available at http://www.geg.com)~~, using either a Blossom 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In yet another preferred embodiment, the percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package (Devereux, J., *et al., Nucleic Acids Res. 12(1)*:387 (1984)) ~~(available at http://www.geg.com)~~, using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. In another embodiment, the percent identity between two amino acid or nucleotide sequences is determined using the algorithm of E. Meyers and W. Miller (CABIOS, 4:11-17 (1989)) which has been incorporated into the ALIGN program (version 2.0), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4.

At page 20, please replace lines 15-27 with the following text:

The nucleic acid and protein sequences of the present invention can further be used as a "query sequence" to perform a search against public databases to, for example, identify other family members or related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul, et al. (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to the nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to the proteins of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al., (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. ~~See http://www.ncbi.nlm.nih.gov.~~

At page 22, please replace lines 9-19 with the following text:

The invention thus also includes polypeptide fragments of the 14273 receptor protein. Fragments can be derived from the amino acid sequence shown in SEQ ID NO:1~~SEQ ID NO 1~~ or SEQ ID NO:4~~SEQ ID NO 4~~. However, the invention also encompasses fragments of the variants of the 14273 receptor protein as described herein.

As used herein, a fragment comprises at least 6 contiguous amino acids from amino acid 1-127 of SEQ ID NO:1 or SEQ ID NO:4, at least 9 amino acids from amino acid 1 to about amino acid 184 of SEQ ID NO:1 or SEQ ID NO:4, greater than 10 amino acids from amino acid 1 to about amino acid 210 of SEQ ID NO:1 or SEQ ID NO:4, and fragments greater than 32 amino acids from amino acid 1 to about amino acid 291 of SEQ ID NO:1 or SEQ ID NO:4. Specific fragments also include fragments greater than those found from amino acid 123-132, 134-141, 162-167, 177-186, 203-237, 238-242, 244-259, 261-292, 295-323, 332-337, 339-345, and 347-351 of SEQ ID NO:1 or SEQ ID NO:4.

At pages 22-23, please replace page 22, line 29 through page 23, line 24 with the following text:

Possible fragments of the human receptor include, but are not limited to: 1) soluble peptides comprising the entire amino terminal extracellular domain about amino acid 1 to about amino acid 45 of SEQ ID NO:1~~SEQ ID NO 1~~, or parts thereof; 2) peptides comprising the entire carboxy terminal intracellular domain from about amino acid 322 to amino acid 361 of SEQ ID NO:1~~SEQ ID NO 1~~, or parts thereof; 3)

peptides comprising the region spanning the entire transmembrane domain from about amino acid 46 to about amino acid 321 of SEQ ID NO:1, or parts thereof; 4) any of the specific transmembrane segments, or parts thereof, from about amino acid 46 to about amino acid 66, from about amino acid 75 to about amino acid 98, from about amino acid 113 to about amino acid 134, from about amino acid 156 to about amino acid 177, from about amino acid 209 to about amino acid 227, from about amino acid 266 to about amino acid 289, and from about amino acid 297 to about amino acid 321 of SEQ ID NO:1; 5) any of the three intracellular or three extracellular loops, or parts thereof, from about amino acid 67 to about amino acid 74, from about amino acid 135 to about amino acid 155, from about amino acid 228 to about amino acid 265, from about amino acid 99 to about amino acid 112, from about amino acid 178 to about amino acid 208, and from about amino acid 290 to about amino acid 296 of SEQ ID NO:1. Fragments further include combinations of the above fragments, such as an amino terminal domain combined with one or more transmembrane segments and the attendant extra or intracellular loops or one or more transmembrane segments, and the attendant intra or extracellular loops, plus the carboxy terminal domain. Thus, any of the above fragments can be combined. Other fragments include the mature protein from about amino acid 37 to 361 of SEQ ID NO:1. Other fragments contain the various functional sites described herein and a sequence containing the GPCR signature sequence. Fragments, for example, can extend in one or both directions from the functional site to encompass 5, 10, 15, 20, 30, 40, 50, or up to 100 amino acids. Further, fragments can include sub-fragments of the specific domains mentioned above, which sub-fragments retain the function of the domain from which they are derived.

At page 41, please replace lines 2-26 with the following text:

Polynucleotides

The nucleotide sequence in SEQ ID NO:2~~SEQ ID NO 2~~ and SEQ ID NO:5~~SEQ ID NO 5~~ was obtained by sequencing the deposited full length cDNA. Accordingly, the sequence of the deposited clone is controlling as to any discrepancies between the two and any reference to the sequence of SEQ ID NO:2~~SEQ ID NO 2~~ and SEQ ID NO:5~~SEQ ID NO 5~~ includes reference to the sequence of the deposited cDNA.

The specifically disclosed cDNA comprises the coding region and 5.· and 3.· untranslated sequences.

The human 14273 receptor cDNA is approximately 1743 nucleotides in length and encodes a full length protein that is approximately 361 amino acid residues in length. The nucleic acid is expressed in fetal brain, heart, skeletal muscle, thymus, prostate, placenta, and uterus. Structural analysis of the amino acid sequence of SEQ ID NO:1~~SEQ ID NO 1~~ and SEQ ID NO:4~~SEQ ID NO 4~~ is provided in Figures 3 and 9, a hydropathy plot. The figures show the putative structure of the seven transmembrane segments, the amino terminal extracellular domain and the carboxy terminal intracellular domain.

As used herein, the term "transmembrane segment" refers to a structural amino acid motif which includes a hydrophobic helix that spans the plasma membrane. The entire transmembrane domain spans from about amino acid 46 to about amino acid 321 of SEQ ID NO:1 or SEQ ID NO:4.
Seven segments span the membrane and there are three intracellular and three extracellular loops in this domain.

The invention provides isolated polynucleotides encoding a 14273 receptor protein. The term "14273 polynucleotide" or "14273 nucleic acid" refers to the sequence shown in SEQ ID NO:2~~SEQ ID NO 2~~ and SEQ ID NO:5~~SEQ ID NO 5~~ or in the deposited cDNA. The term "receptor polynucleotide" or "receptor nucleic acid" further includes variants and fragments of the 14273 polynucleotide.

At page 43, please replace lines 9-16 with the following text:

One receptor nucleic acid comprises the nucleotide sequence shown in SEQ ID NO:2~~SEQ ID NO 2~~, corresponding to human brain cDNA or the murine ortholog shown in SEQ ID NO:5~~SEQ ID NO 5~~.

In one embodiment, the receptor nucleic acid comprises only the coding region.

The invention further provides variant receptor polynucleotides, and fragments thereof, that differ from the nucleotide sequence shown in SEQ ID NO:2~~SEQ ID NO 2~~ or SEQ ID NO:5~~SEQ ID NO 5~~ due to degeneracy of the genetic code and thus encode the same protein as that encoded by the nucleotide sequence shown in SEQ ID NO:2~~SEQ ID NO 2~~ or SEQ ID NO:5~~SEQ ID NO 5~~.

At pages 43-44, please replace page 43, line 27 through page 44, line 25 with the following text:

Orthologs, homologs, and allelic variants can be identified using methods well known in the art. These variants comprise a nucleotide sequence encoding a receptor that is 50%, at least about 55%, typically at least about 70-75%, more typically at least about 80-85%, and most typically at least about 90-95% or more homologous to the nucleotide sequence shown in SEQ ID NO:2~~SEQ ID NO 2~~ or SEQ ID NO:5~~SEQ ID NO 5~~ or a fragment of this sequence. Such nucleic acid molecules can readily be identified as being able to hybridize under stringent conditions, to the nucleotide sequence shown in SEQ ID NO:2~~SEQ ID NO 2~~ or SEQ ID NO:5~~SEQ ID NO 5~~ or a fragment of the sequence. It is understood that stringent hybridization does not indicate substantial homology where it is due to general homology, such as poly A sequences, or sequences common to all or most proteins, all GPCRs, or all family I GPCRs or sequences found dispersed throughout the genome that are not specific to any genes, for example, homopolymer stretches. Moreover, it is understood that variants do not include any of the nucleic acid sequences that may have been disclosed

prior to the invention. Preferred variants include those that are correlated with hypertrophy of cardiac myocytes and with congestive heart failure.

As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences encoding a receptor at least 50%, 55% homologous to each other typically remain hybridized to each other. The conditions can be such that sequences at least about 65%, at least about 70%, or at least about 75% or more homologous to each other typically remain hybridized to each other. Such stringent conditions are known to those skilled in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. One example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45□C, followed by one or more washes in 0.2 X SSC, 0.1% SDS at 50-65□C. In one embodiment, an isolated receptor nucleic acid molecule that hybridizes under stringent conditions to the sequence of SEQ ID NO:2~~SEQ ID NO 2~~ corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural protein).

At page 45, please replace lines 1-22 with the following text:

In one embodiment, an isolated receptor nucleic acid fragment is at least 5 nucleotides in length and is derived from the sequence from 1-410, 118-1295, or 1630-1743 nucleotides in length and hybridizes under stringent conditions to the nucleotide molecule comprising the nucleotide sequence of SEQ ID NO:2~~SEQ ID NO 2~~ or SEQ ID NO:5 ~~SEQ ID NO 5~~. In other embodiments, the nucleic acid is at least 10, 15, 20, 30, 40, 50, 100, 250, or 500 nucleotides in length or greater.

In another embodiment, the fragment comprises contiguous nucleotides from around 410 to around 442 of SEQ ID NO:2 or SEQ ID NO:5 that are greater than 13, 442-473 of SEQ ID NO:2 or SEQ ID NO:5 that are greater than 26, 605-745 that are greater than 44, 745-857 of SEQ ID NO:2 or SEQ ID NO:5 that are greater than 17, 857-924 of SEQ ID NO:2 or SEQ ID NO:5 that are greater than 23, 925-1118 of SEQ ID NO:2 or SEQ ID NO:5 that are greater than 23, and 1295-1630 of SEQ ID NO:2 or SEQ ID NO:5 that are greater than 25.

In another embodiment an isolated receptor nucleic acid encodes the entire coding region from amino acid 1 to amino acid 321 of SEQ ID NO:1 or SEQ ID NO:4. In another embodiment the isolated receptor nucleic acid encodes a sequence corresponding to the mature protein from about amino acid 36 to amino acid 321 of SEQ ID NO:1 or SEQ ID NO:4. Other fragments include nucleotide sequences that include part, or all, of the coding region and extend into either the 5.· or 3.· noncoding region, or both of these regions. Other fragments include nucleotide sequences encoding the amino acid fragments described

herein. Further fragments can include subfragments of the specific domains or sites described herein. Fragments also include nucleic acid sequences corresponding to specific amino acid sequences described above or fragments thereof. Nucleic acid fragments, according to the present invention, are not to be construed as encompassing those fragments that may have been disclosed prior to the invention.

At page 46, please replace lines 1-12 with the following text:

Receptor nucleic acid fragments include nucleic acid molecules encoding a polypeptide comprising the amino terminal extracellular domain including amino acid residues from 1 to about 45 of SEQ ID NO:1 or SEQ ID NO:4, a polypeptide comprising the region spanning the transmembrane domain (amino acid residues from about 46 to about 321 of SEQ ID NO:1 or SEQ ID NO:4), a polypeptide comprising the carboxy terminal intracellular domain (amino acid residues from about 322 to about 361 of SEQ ID NO:1 or SEQ ID NO:4), and a polypeptide encoding the G-protein receptor signature (135-136 or surrounding amino acid residues from about 125 to about 145 of SEQ ID NO:1 or SEQ ID NO:4), nucleic acid molecules encoding any of the seven transmembrane segments, extracellular or intracellular loops, glycosylation, phosphorylation, myristoylation, and amidation sites. Where the location of the domains have been predicted by computer analysis, one of ordinary skill would appreciate that the amino acid residues constituting these domains can vary depending on the criteria used to define the domains.

At page 46, please replace lines 22-27 with the following text:

A probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 10, 12, typically about 25, more typically about 40, 50 or 75 consecutive nucleotides of SEQ ID NO:2~~SEQ ID NO 2~~ or SEQ ID NO:5 ~~SEQ ID NO 5~~sense or anti-sense strand or other receptor polynucleotides. A probe further comprises a label, e.g., radioisotope, fluorescent compound, enzyme, or enzyme co-factor.

At page 47, please replace lines 19-28 with the following text:

The receptor polynucleotides are useful as a hybridization probe for cDNA and genomic DNA to isolate a full-length cDNA and genomic clones encoding the polypeptide described in SEQ ID NO:1~~SEQ ID~~

~~NO 1~~ or SEQ ID NO:4~~SEQ ID NO 4~~ and to isolate cDNA and genomic clones that correspond to variants producing the same polypeptide shown in SEQ ID NO:1~~SEQ ID NO 1~~ or SEQ ID NO:4~~SEQ ID NO 4~~ or the other variants described herein. Variants can be isolated from the same tissue and organism from which the polypeptide shown in SEQ ID NO:1~~SEQ ID NO 1~~ or SEQ ID NO:4~~SEQ ID NO 4~~ was isolated, different tissues from the same organism, or from different organisms. This method is useful for isolating genes and cDNA that are developmentally-controlled and therefore may be expressed in the same tissue or different tissues at different points in the development of an organism.

At page 48, please replace lines 5-8 with the following text:

The nucleic acid probe can be, for example, the full-length cDNA of SEQ ID NO:1~~SEQ ID NO 1~~ or SEQ ID NO:4~~SEQ ID NO 4~~, or a fragment thereof, such as an oligonucleotide of at least 10, 12, 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to mRNA or DNA.

At page 56, please replace lines 20-24 with the following text:

Examples of antisense molecules useful to inhibit nucleic acid expression include antisense molecules complementary to a fragment of the 5.' untranslated region of SEQ ID NO:2~~SEQ ID NO 2~~ or SEQ ID NO:5~~SEQ ID NO 5~~ which also includes the start codon and antisense molecules which are complementary to a fragment of the 3.' untranslated region of SEQ ID NO:2~~SEQ ID NO 2~~ or SEQ ID NO:5~~SEQ ID NO 5~~.